

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/582,304  
Source: 1 FWP  
Date Processed by STIC: 6/21/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/582,304

TIME: 11:06:58

Input Set : A:\14875-166US1.txt

Output Set: N:\CRF4\06212006\J582304.raw

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3 <110> APPLICANT: Kimura, Naoki
4     Tsuchiya, Masayuki
5     Nanami, Masahiko
6     Tomimatsu, Takashi
7     Kawai, Shigeto
9 <120> TITLE OF INVENTION: Cell Death Inducing Agents
11 <130> FILE REFERENCE: 14875-166US1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/582,304
C--> 13 <141> CURRENT FILING DATE: 2006-06-09
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/018501
14 <151> PRIOR FILING DATE: 2004-12-10
16 <150> PRIOR APPLICATION NUMBER: JP 2003-415758
17 <151> PRIOR FILING DATE: 2003-12-12
19 <160> NUMBER OF SEQ ID NOS: 20
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1572
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (14)..(1561)
31 <223> OTHER INFORMATION:
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35           Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser
36           1           5           10
38 ata act gca ggt gtc cat tgc cag gtc cag ttg cag cag tct gga cct      97
39 Ile Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro
40           15           20           25
42 gag ctg gtg aag cct ggg gct tca gtg aag atg tct tgt aag gct tct      145
43 Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
44           30           35           40
46 ggc tac acc ttc aca gac tac ttt ata cac tgg gtg aaa cag agg cct      193
47 Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro
48 45           50           55           60
50 gga cag gga ctt gaa tgg att gga tgg att ttt cct gga gat gat act      241
51 Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr
52           65           70           75
54 act gat tac aat gag aag ttc agg ggc aag acc aca ctg act gca gac      289
55 Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp
56           80           85           90
58 aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag      337

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59	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	
60			95					100					105				
62	gac	tct	gcg	atg	tat	ttc	tgt	gta	agg	agt	gac	gac	ttt	gac	tac	tgg	385
63	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Val	Arg	Ser	Asp	Asp	Phe	Asp	Tyr	Trp	
64		110					115					120					
66	ggc	cag	ggc	acc	act	ctc	aca	gtc	tcc	tca	ggg	gga	ggc	ggg	tca	ggc	433
67	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
68	125					130					135					140	
70	gga	ggg	ggc	tct	ggc	ggg	ggc	gga	agc	caa	att	gtt	ctc	acc	cag	tgc	481
71	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	
72				145						150					155		
74	cca	gca	atc	atg	tct	gca	tct	cca	ggg	gag	aag	gtc	acc	ata	acc	tgc	529
75	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	
76				160					165					170			
78	agt	gcc	agc	tca	agt	gta	agt	tac	atg	cac	tgg	ttc	cag	cag	aag	cca	577
79	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	
80			175					180					185				
82	ggc	act	ttt	ccc	aaa	ctc	tgg	att	tat	agc	aca	tcc	aac	ctg	gct	tct	625
83	Gly	Thr	Phe	Pro	Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	
84		190					195					200					
86	gga	gtc	cct	act	cgc	ttc	agt	ggc	agt	gga	tct	ggg	acc	tct	tac	tct	673
87	Gly	Val	Pro	Thr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	
88	205					210					215					220	
90	ctc	aca	atc	agc	cga	atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	721
91	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
92				225						230					235		
94	cag	caa	agg	acg	agt	tat	cca	ccc	acg	ttc	ggc	tcg	ggg	aca	aag	ttg	769
95	Gln	Gln	Arg	Thr	Ser	Tyr	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	
96			240						245				250				
98	gag	ata	aaa	gga	ggg	ggg	ggc	agt	ggg	ggc	ggc	gga	tcc	ggg	ggc	ggg	817
99	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
100			255					260					265				
102	ggc	tca	cag	gtc	cag	ttg	cag	cag	tct	gga	cct	gag	ctg	gtg	aag	cct	865
103	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	
104		270					275					280					
106	ggg	gct	tca	gtg	aag	atg	tct	tgt	aag	gct	tct	ggc	tac	acc	ttc	aca	913
107	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
108	285					290					295					300	
110	gac	tac	ttt	ata	cac	tgg	gtg	aaa	cag	agg	cct	gga	cag	gga	ctt	gaa	961
111	Asp	Tyr	Phe	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	
112				305						310					315		
114	tgg	att	gga	tgg	att	ttt	cct	gga	gat	gat	act	act	gat	tac	aat	gag	1009
115	Trp	Ile	Gly	Trp	Ile	Phe	Pro	Gly	Asp	Asp	Thr	Thr	Asp	Tyr	Asn	Glu	
116			320						325				330				
118	aag	ttc	agg	ggc	aag	acc	aca	ctg	act	gca	gac	aaa	tcc	tcc	agc	aca	1057
119	Lys	Phe	Arg	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	
120			335					340					345				
122	gcc	tac	att	ttg	ctc	agc	agc	ctg	acc	tct	gag	gac	tct	gcg	atg	tat	1105
123	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Met	Tyr	

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124      350      355      360
126 ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc act      1153
127 Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr
128 365      370      375      380
130 ctc aca gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc      1201
131 Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
132      385      390      395
134 ggt ggc gga agc caa att gtt ctc acc cag tcg cca gca atc atg tct      1249
135 Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser
136      400      405      410
138 gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt      1297
139 Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser
140      415      420      425
142 gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa      1345
143 Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys
144      430      435      440
146 ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc      1393
147 Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg
148 445      450      455      460
150 ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga      1441
151 Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
152      465      470      475
154 atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt      1489
155 Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser
156      480      485      490
158 tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa gac tac      1537
159 Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr
160      495      500      505
162 aag gat gac gac gat aag tga taa gcggccgcaa t      1572
163 Lys Asp Asp Asp Asp Lys
164      510
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 514
169 <212> TYPE: PRT
170 <213> ORGANISM: Mus musculus
172 <400> SEQUENCE: 2
173 Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
174 1      5      10      15
176 Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
177      20      25      30
179 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
180      35      40      45
182 Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
183      50      55      60
185 Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
186 65      70      75      80
188 Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
189      85      90      95
191 Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met

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192          100          105          110
194 Tyr  Phe  Cys  Val  Arg  Ser  Asp  Asp  Phe  Asp  Tyr  Trp  Gly  Gln  Gly  Thr
195          115          120          125
197 Thr  Leu  Thr  Val  Ser  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser
198          130          135          140
200 Gly  Gly  Gly  Gly  Ser  Gln  Ile  Val  Leu  Thr  Gln  Ser  Pro  Ala  Ile  Met
201 145          150          155          160
203 Ser  Ala  Ser  Pro  Gly  Glu  Lys  Val  Thr  Ile  Thr  Cys  Ser  Ala  Ser  Ser
204          165          170          175
206 Ser  Val  Ser  Tyr  Met  His  Trp  Phe  Gln  Gln  Lys  Pro  Gly  Thr  Phe  Pro
207          180          185          190
209 Lys  Leu  Trp  Ile  Tyr  Ser  Thr  Ser  Asn  Leu  Ala  Ser  Gly  Val  Pro  Thr
210          195          200          205
212 Arg  Phe  Ser  Gly  Ser  Gly  Ser  Gly  Thr  Ser  Tyr  Ser  Leu  Thr  Ile  Ser
213          210          215          220
215 Arg  Met  Glu  Ala  Glu  Asp  Ala  Ala  Thr  Tyr  Tyr  Cys  Gln  Gln  Arg  Thr
216 225          230          235          240
218 Ser  Tyr  Pro  Pro  Thr  Phe  Gly  Ser  Gly  Thr  Lys  Leu  Glu  Ile  Lys  Gly
219          245          250          255
221 Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gln  Val
222          260          265          270
224 Gln  Leu  Gln  Gln  Ser  Gly  Pro  Glu  Leu  Val  Lys  Pro  Gly  Ala  Ser  Val
225          275          280          285
227 Lys  Met  Ser  Cys  Lys  Ala  Ser  Gly  Tyr  Thr  Phe  Thr  Asp  Tyr  Phe  Ile
228          290          295          300
230 His  Trp  Val  Lys  Gln  Arg  Pro  Gly  Gln  Gly  Leu  Glu  Trp  Ile  Gly  Trp
231 305          310          315          320
233 Ile  Phe  Pro  Gly  Asp  Asp  Thr  Thr  Asp  Tyr  Asn  Glu  Lys  Phe  Arg  Gly
234          325          330          335
236 Lys  Thr  Thr  Leu  Thr  Ala  Asp  Lys  Ser  Ser  Ser  Thr  Ala  Tyr  Ile  Leu
237          340          345          350
239 Leu  Ser  Ser  Leu  Thr  Ser  Glu  Asp  Ser  Ala  Met  Tyr  Phe  Cys  Val  Arg
240          355          360          365
242 Ser  Asp  Asp  Phe  Asp  Tyr  Trp  Gly  Gln  Gly  Thr  Thr  Leu  Thr  Val  Ser
243          370          375          380
245 Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser
246 385          390          395          400
248 Gln  Ile  Val  Leu  Thr  Gln  Ser  Pro  Ala  Ile  Met  Ser  Ala  Ser  Pro  Gly
249          405          410          415
251 Glu  Lys  Val  Thr  Ile  Thr  Cys  Ser  Ala  Ser  Ser  Ser  Val  Ser  Tyr  Met
252          420          425          430
254 His  Trp  Phe  Gln  Gln  Lys  Pro  Gly  Thr  Phe  Pro  Lys  Leu  Trp  Ile  Tyr
255          435          440          445
257 Ser  Thr  Ser  Asn  Leu  Ala  Ser  Gly  Val  Pro  Thr  Arg  Phe  Ser  Gly  Ser
258          450          455          460
260 Gly  Ser  Gly  Thr  Ser  Tyr  Ser  Leu  Thr  Ile  Ser  Arg  Met  Glu  Ala  Glu
261 465          470          475          480
263 Asp  Ala  Ala  Thr  Tyr  Cys  Gln  Gln  Arg  Thr  Ser  Tyr  Pro  Pro  Thr
264          485          490          495

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266 Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp  
 267                   500                   505                   510  
 269 Asp Lys  
 273 <210> SEQ ID NO: 3  
 274 <211> LENGTH: 5  
 275 <212> TYPE: PRT  
 276 <213> ORGANISM: Mus musculus  
 278 <400> SEQUENCE: 3  
 279 Asp Tyr Phe Ile His  
 280 1                   5  
 283 <210> SEQ ID NO: 4  
 284 <211> LENGTH: 17  
 285 <212> TYPE: PRT  
 286 <213> ORGANISM: Mus musculus  
 288 <400> SEQUENCE: 4  
 289 Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg  
 290 1                   5                   10                   15  
 292 Gly  
 296 <210> SEQ ID NO: 5  
 297 <211> LENGTH: 6  
 298 <212> TYPE: PRT  
 299 <213> ORGANISM: Mus musculus  
 301 <400> SEQUENCE: 5  
 302 Ser Asp Asp Phe Asp Tyr  
 303 1                   5  
 306 <210> SEQ ID NO: 6  
 307 <211> LENGTH: 10  
 308 <212> TYPE: PRT  
 309 <213> ORGANISM: Mus musculus  
 311 <400> SEQUENCE: 6  
 312 Ser Ala Ser Ser Ser Val Ser Tyr Met His  
 313 1                   5                   10  
 316 <210> SEQ ID NO: 7  
 317 <211> LENGTH: 7  
 318 <212> TYPE: PRT  
 319 <213> ORGANISM: Mus musculus  
 321 <400> SEQUENCE: 7  
 322 Ser Thr Ser Asn Leu Ala Ser  
 323 1                   5  
 326 <210> SEQ ID NO: 8  
 327 <211> LENGTH: 9  
 328 <212> TYPE: PRT  
 329 <213> ORGANISM: Mus musculus  
 331 <400> SEQUENCE: 8  
 333 Gln Gln Arg Thr Ser Tyr Pro Pro Thr  
 334 1                   5  
 337 <210> SEQ ID NO: 9  
 338 <211> LENGTH: 402  
 339 <212> TYPE: DNA

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/582,304

DATE: 06/21/2006  
TIME: 11:06:59

Input Set : A:\14875-166US1.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:15,16,17,18,19,20

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/582,304

DATE: 06/21/2006

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Input Set : A:\14875-166US1.txt

Output Set: N:\CRF4\06212006\J582304.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31  
L:347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:345  
L:429 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:427  
L:504 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:502  
L:640 M:112 C: (48) String data converted to lower case,